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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/525,831	10/17/2005	Tetsuya Nakatsura	P26795	5642

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EXAMINER

HOLLERAN, ANNE L

ART UNIT	PAPER NUMBER
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1643

NOTIFICATION DATE	DELIVERY MODE
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01/04/2008

ELECTRONIC

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

gbpatent@gbpatent.com
pto@gbpatent.com

Office Action Summary

Application No.

10/525,831

Applicant(s)

NAKATSURA ET AL.

Examiner

Anne L. Holleran

Art Unit

1643

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 19 October 2007.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-26 is/are pending in the application.
- 4a) Of the above claim(s) 1-8, 11-20 and 25 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☐ Claim(s) _____ is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
- Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
- Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☒ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO/SB/08)
Paper No(s)/Mail Date 1/06, 4/06.
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____.
- 5) ☐ Notice of Informal Patent Application
- 6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

1. Applicant's election with traverse of Group II (claims 9-10, 21-23, 24 and 26) and further elect species of SEQ ID NO: 14 in the reply filed on 10/19/2007 is acknowledged. The traversal is on the ground(s) that the examiner has not set forth any reason as to why the species are not so linked, and that the restriction should be withdrawn for this reason alone. This is not found persuasive because the restriction is between groups I, II, III, IV and V, and the reasons set forth are given in the previous Office action, in which it was set forth that a polypeptide comprising the amino acid sequence of SEQ ID NO: 1 is taught in the prior art by Old (WO 99/04265), and therefore the polypeptide of SEQ ID NO: 1 is not a special technical feature. Additionally, it was noted that the claims recited 20 additional peptide sequences (SEQ ID NO: 3 through SEQ ID NO: 22), and the examiner requested an election of species of one of them to begin the examination process. A restriction between species will be withdrawn if a generic claim is found to be allowable. The reason for the lack of unity between the species was stated in the previous Office action, because the Office action contained the statement that each of the peptide sequences SEQ ID NO: 3 through SEQ ID NO: 22 is an individual species of peptide. Applicants have not answered this assertion by stating on the record whether in fact these peptides share a common structural feature. Applicants also noted that a search of group I and group II would overlap and therefore search and examination of both groups would not impose a serious burden on the examiner. This is not found persuasive because group I is drawn to polypeptide claims and group II is drawn to polynucleotide claims. Examination of polypeptide

claims requires consideration of a different set of issues than does examination of polynucleotide claims, as each of these products may be used in different methods, requiring search of different fields of the non-patent literature. Furthermore, while a polynucleotide may be a novel product, the protein that it encodes may be already known in the art and not disclosed in the same databases as those that are searched in the examination of polynucleotides. Lastly, burden is not considered in the analysis of lack of unity under PCT Rule 13.1. Therefore, applicants' traverse of the restriction requirement is not persuasive.

The requirement is still deemed proper and is therefore made FINAL.

2. Claims 1-26 are pending. Claims 1-8, 11-20, and 25 are withdrawn from consideration. Claims 9, 10, 21-24 and 26 are examined on the merits.

Claim Objections

3. Claim 9 is objected to for depending from a withdrawn claim. Claim 9 should be rewritten to include all of the limitations recited in claim 1.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

4. Claim 10 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 10 is indefinite because the scope of the claim cannot be determined with respect to the section "b", which recites a DNA hybridizing with the DNA having the nucleotide sequence shown in SEQ ID NO: 2 under stringent conditions. The conditions that define "stringent conditions" are not set out in the specification, merely an example of such conditions (page 11, last paragraph). Therefore, it is not possible to discern which nucleic acids are included within the scope of the claim and which are not included.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

5. Claim 10 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The basis for this rejection is that a DNA hybridizing with the DNA having the nucleotide sequence shown in SEQ ID NO: 2 under stringent conditions and encoding a protein having immune-stimulating activity, or DNA having a partial sequence of the DNA of SEQ ID NO: 2 or of a sequence that hybridizes with SEQ ID NO: 2 and encoding a protein having immune-stimulating activity each encompass a genus of nucleic acids for which the disclosure of SEQ ID NO: 2 is not representative.

For a claim drawn to a genus, the written description requirement may be satisfied through sufficient description of a representative number of species by actual reduction to

practice or by disclosure of relevant, identifying characteristics, i.e. structure or other physical and/or chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show the applicant was in possession of the claimed genus. A "representative number of species" means that the species, which are adequately described, are representative of the entire genus. Thus, when there is substantial variation within the genus, one must describe a sufficient variety of species to reflect the variation within the genus (see Official Gazette 1241 OG 174, January 30, 2001).

In the present case, the genus encompassed by a DNA hybridizing with a DNA having the nucleotide sequence shown in SEQ ID NO: 2 under stringent conditions, and encoding a protein having immune stimulating activity is a very different nucleotide sequence from SEQ ID NO: 2 itself and encodes a protein that is very different from the one encoded by SEQ ID NO: 2. Hybridization under stringent conditions does not limit the size of the nucleotides and because the reference nucleotide sequence is one that "comprises SEQ ID NO: 2" the hybridization could occur over regions that are outside of SEQ ID NO: 2 and therefore, have no sequence relationship with SEQ ID NO: 2 at all. The genus encompassed by a DNA having a partial sequence of DNA having the nucleotide sequence of SEQ ID NO: 2 is a varied genus and includes DNA molecules that encode any number of proteins, because almost any protein is one that has immune-stimulating activity. A partial sequence may be as small as 2 nucleotides in length. Therefore, a DNA having (interpret as "comprising") a partial sequence may be one that has only a sequence of 2 nucleotides in common with SEQ ID NO: 2. Therefore, it does not appear that the disclosure of SEQ ID NO: 2 itself is representative of the broad scope

encompassed either by a DNA hybridizing with the DNA having a nucleotide sequence shown in SEQ ID NO: 2 under stringent conditions, or a DNA having a partial sequence SEQ ID NO: 2 and encoding a protein having immune-stimulating activity.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

The changes made to 35 U.S.C. 102(e) by the American Inventors Protection Act of 1999 (AIPA) and the Intellectual Property and High Technology Technical Amendments Act of 2002 do not apply when the reference is a U.S. patent resulting directly or indirectly from an international application filed before November 29, 2000. Therefore, the prior art date of the reference is determined under 35 U.S.C. 102(e) prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. 102(e)).

6. Claims 9, 10, 21-24 and 26 are rejected under 35 U.S.C. 102(b) as being anticipated WO 99/04265 (Old, L. J. et al., published 28 January 1999; cited in IDS) as evidenced by Accession No. AAX40073 (12 July 1999, WO 99/04265-A2, Database N_Geneseq_200701).

Claim 9 is drawn to a DNA encoding the cancer antigen of claim 1, which is a polypeptide that comprises the amino acid sequence of SEQ ID NO: 1 or comprises a sequence that has changes such as additions, subtractions, substitutions, insertions of one or several amino acids and encodes a protein with immune stimulating activity. The specification at page 7, lines 4-8 defines a “protein having immune-stimulating activity” to mean a “protein having activity of inducing an immune response such as generation of an antibody or cell-mediated immunity. Among them, a protein having T cell-stimulating activity of stimulating cytotoxic T lymphocytes (killer T cells/CTL) is particular preferable”. Claim is drawn, in the alternative, to a DNA having the nucleotide sequence shown in SEQ ID NO: 2, a DNA hybridizing with the DNA having the nucleotide sequence shown in SEQ ID NO: 2 under stringent conditions, and encoding a protein having immune-stimulating activity, or a DNA having a partial sequence of either of the previous DNA molecules and encoding a protein having immune-stimulating activity. Claim 21 is drawn to a cancer vaccine, which comprises the DNA of claim 9, or recombinant virus, or recombinant bacteria comprising said DNA. Claim 22 is the cancer vaccine of claim 21 which further comprises an adjuvant. The phrase “cancer vaccine” is interpreted as an intended use for claim 21 respect to the aspect of the claim where the product is simply a DNA of claim 9. Claim 23 is drawn to a probe for diagnosing cancers, which comprises the DNA of claim 9, where the term “probe” does not appears to change the structure of the claimed nucleic acid and is therefore considered a term of intended use, not affecting the scope of the claim. Claim 24 is drawn to an agent for diagnosing cancers, which comprises the cancer diagnostic probe of claim 23 and /or an antibody. Claim 26 is drawn to a probe of claim 23, where claim lists, in the alternative, cancers that may be diagnosed with the probe.

WO 99/04265 teaches nucleotide sequence that encodes the polypeptide having the amino acid sequence of SEQ ID NO: 1 as evidenced by accession no. AAX40073, which shows the alignment between a nucleotide sequence of WO 99/04265, encoding a colon cancer associated gene and the polypeptide sequence of SEQ ID NO: 1. Accession no. AAX40073 teaches that the nucleic acid of WO 99/04265 is 3309 base pairs, which is a nucleic acid molecule described in WO 99/04265 as SEQ ID NO: 582, translated as SEQ ID NO: 583 (see page 62, lines 21-26). WO 99/04265 also teaches that the nucleic acids described therein maybe comprised within pharmaceutical compositions (see page 6, lines 5-11) and that the pharmaceutical compositions may further comprise an adjuvant (see page 6, lines 27-28). Therefore, WO 99/04265 teaches nucleic acids and compositions as claimed.

7. Claims 9, 10, 21, 23, 24 and 26 are rejected under 35 U.S.C. 102(b) as being anticipated by Scanlan (US 6,403,373; issued Jun. 11, 2002).

Scanlan teaches and claims SEQ ID NO: 18, which is a nucleic acid sequence that encodes a protein that comprises the sequence of SEQ ID NO: 1, and is an antigen that is associated with colon cancer. See below for the alignment of SEQ ID NO: 1 with nucleic acid of Scanlan from US 6517837, which is a divisional of the application that resulted in US 6,403,373:

```
RESULT 5
US-09-510-543-18
; Sequence 18, Application US/09510543
; Patent No. 6517837
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED WITH COLON CANCER AND
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING COLON CANCER
; FILE REFERENCE: LUD-5506.1-JEL/NDH
; CURRENT APPLICATION NUMBER: US/09/510,543
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 09/102,322
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; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 18
; LENGTH: 5878
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2237..2237
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 2260..2260
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 2305..2305
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 2315..2315
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 2355..2355
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 2420..2420
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 2421..2421
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 2423..2423
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 2490..2490
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 2523..2523
; OTHER INFORMATION:
US-09-510-543-18
```

Alignment Scores:

Pred. No.:	0	Length:	5878
Score:	4450.00	Matches:	858
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-525-831-1 (1-858) x US-09-510-543-18 (1-5878)

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Qy      1 MetSerValValGlyLeuAspValGlySerGlnSerCysTyrIleAlaValAlaArgAla 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2612 ATGTCGGTGGTGGGGTTGGACGTGGGCTCGCAGAGCTGCTACATCGCGGTAGCCCGGGCC 2671

Qy      21 GlyGlyIleGluThrIleAlaAsnGluPheSerAspArgCysThrProSerValIleSer 40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2672 GGGGGCATCGAGACCATCGCCAATGAGTTGACGACCGGTGCACCCCGTCAGTCATATCA 2731

Qy      41 PheGlySerLysAsnArgThrIleGlyValAlaAlaLysAsnGlnGlnIleThrHisAla 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2732 TTTGGATCAAAAAATAGAACAATCGGAGTTGCAGCCAAAAATCAGCAAATCACTCATGCA 2791

Qy      61 AsnAsnThrValSerAsnPheLysArgPheHisGlyArgAlaPheAsnAspProPheIle 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2792 AACAAATACGGTGTCTAACTTCAAAGATTTCATGGCCGAGCATTCAATGACCCCTTCATT 2851

Qy      81 GlnLysGluLysGluAsnLeuSerTyrAspLeuValProLeuLysAsnGlyGlyValGly 100
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      |||
Db      2852 CAAAAGGAGAAGGAAAACCTTGAGTTACGATTTGGTTCATTGAAAAATGGTGGAGTTGGA 2911
Qy      101 IleLysValMetTyrMetGlyGluGluHisLeuPheSerValGluGlnIleThrAlaMet 120
      |||
Db      2912 ATAAAGGTAATGTACATGGGTGAAGAACATCTATTTAGTGTGGAGCAGATAACAGCCATG 2971
Qy      121 LeuLeuThrLysLeuLysGluThrAlaGluAsnSerLeuLysLysProValThrAspCys 140
      |||
Db      2972 TTGTTGACTAAGCTGAAGGAACTGCTGAAAAACAGCCTCAAGAAACCAGTAACAGATTGT 3031
Qy      141 ValIleSerValProSerPhePheThrAspAlaGluArgArgSerValLeuAspAlaAla 160
      |||
Db      3032 GTTATTTTCAGTCCCCCTCTTCTTTACAGATGCTGAGAGGCGATCTGTGTTAGATGCTGCA 3091
Qy      161 GlnIleValGlyLeuAsnCysLeuArgLeuMetAsnAspMetThrAlaValAlaLeuAsn 180
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Db      3092 CAGATTGTTGGCCTAACTGTTTAAGACTTATGAATGACATGACAGCTGTTGCTTTGAAT 3151
Qy      181 TyrGlyIleTyrLysGlnAspLeuProSerLeuAspGluLysProArgIleValValPhe 200
      |||
Db      3152 TACGGAATTTATAAGCAGGATCTCCCAAGCCTGGATGAGAAACCTCGGATAGTGGTTTTT 3211
Qy      201 ValAspMetGlyHisSerAlaPheGlnValSerAlaCysAlaPheAsnLysGlyLysLeu 220
      |||
Db      3212 GTTGATATGGGACATTCAGCTTTTCAAGTGTCTGCTTGTGCTTTTAAACAGGGAAAATTG 3271
Qy      221 LysValLeuGlyThrAlaPheAspProPheLeuGlyGlyLysAsnPheAspGluLysLeu 240
      |||
Db      3272 AAGGTACTGGGAACAGCTTTTGATCCTTCTTAGGAGGAAAAAAGCTTCGATGAAAAGTTA 3331
Qy      241 ValGluHisPheCysAlaGluPheLysThrLysTyrLysLeuAspAlaLysSerLysIle 260
      |||
Db      3332 GTGGAACATTTTGTGCAGAATTTAAACTAAGTACAAGTTGGATGCAAAATCCAAATA 3391
Qy      261 ArgAlaLeuLeuArgLeuTyrGlnGluCysGluLysLeuLysLysLeuMetSerSerAsn 280
      |||
Db      3392 CGAGCACTCCTACGTCTGTATCAGGAATGTGAAAACTGAAAAAGCTAATGAGCTCTAAC 3451
Qy      281 SerThrAspLeuProLeuAsnIleGluCysPheMetAsnAspLysAspValSerGlyLys 300
      |||
Db      3452 AGCACAGACCTTCCACTGAATATCGAATGCTTTATGAATGATAAAGATGTTTCCGGAAAG 3511
Qy      301 MetAsnArgSerGlnPheGluGluLeuCysAlaGluLeuLeuGlnLysIleGluValPro 320
      |||
Db      3512 ATGAACAGGTACAATTTGAAGAACTCTGTGCTGAACCTCTGCAAAAGATAGAAGTACCC 3571
Qy      321 LeuTyrSerLeuLeuGluGlnThrHisLeuLysValGluAspValSerAlaValGluIle 340
      |||
Db      3572 CTTTATTCACGTGTTGGAACAACTCATCTCAAAGTAGAAGATGTGAGTGCAGTTGAGATT 3631
Qy      341 ValGlyGlyAlaThrArgIleProAlaValLysGluArgIleAlaLysPhePheGlyLys 360
      |||
Db      3632 GTTGGAGGCGCTACACGAATCCAGCTGTGAAGGAAAGAAATGCCAAATTCCTTGAAAA 3691
Qy      361 AspIleSerThrThrLeuAsnAlaAspGluAlaValAlaArgGlyCysAlaLeuGlnCys 380
      |||
Db      3692 GATATTAGCACAACTCAATGCAGATGAAGCAGTAGCCAGAGGATGTGCATTACAGTGT 3751
Qy      381 AlaIleLeuSerProAlaPheLysValArgGluPheSerValThrAspAlaValProPhe 400
      |||
Db      3752 GCAATACTTTCCCGGCATTTAAAGTTAGAGAATTTCCGTCACAGATGCAGTTCCTTTT 3811
Qy      401 ProIleSerLeuIleTrpAsnHisAspSerGluAspThrGluGlyValHisGluValPhe 420
      |||
Db      3812 CCAATATCTCTGATCTGGAACCATGATTCAGAAGATACTGAAGGTGTTTCATGAAGTCTTT 3871

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Qy	421	SerArgAsnHisAlaAlaProPheSerLysValLeuThrPheLeuArgGlyProPhe	440
Db	3872	AGTCGAAACCATGCTGCTCCTTTCTCCAAAGTTCTCACCTTTCTGAGAAGGGGGCCTTTT	3931
Qy	441	GluLeuGluAlaPheTyrSerAspProGlnGlyValProTyrProGluAlaLysIleGly	460
Db	3932	GAGCTAGAAGCTTTCTATTCTGATCCCCAAGGAGTTCCATATCCAGAAGCAAAAATAGGC	3991
Qy	461	ArgPheValValGlnAsnValSerAlaGlnLysAspGlyGluLysSerArgValLysVal	480
Db	3992	CGCTTTGTAGTTTCAGAATGTTTCTGCACAGAAAGATGGAGAAAAATCTAGAGTAAAAGTC	4051
Qy	481	LysValArgValAsnThrHisGlyIlePheThrIleSerThrAlaSerMetValGluLys	500
Db	4052	AAAGTGCAGAGTCAACACCCATGGCATTTTCACCATCTCTACGGCATCTATGGTGGAGAAA	4111
Qy	501	ValProThrGluGluAsnGluMetSerSerGluAlaAspMetGluCysLeuAsnGlnArg	520
Db	4112	GTCCCAACTGAGGAGAATGAAATGTCCTTCTGAAGCTGACATGGAGTGTCTGAATCAGAGA	4171
Qy	521	ProProGluAsnProAspThrAspLysAsnValGlnGlnAspAsnSerGluAlaGlyThr	540
Db	4172	CCACCAGAAAAACCAGACACTGATAAAAAATGTCCAGCAAGACAACAGTGAAGCTGGAACA	4231
Qy	541	GlnProGlnValGlnThrAspAlaGlnGlnThrSerGlnSerProProSerProGluLeu	560
Db	4232	CAGCCCCAGGTACAAACTGATGCTCAACAAACCTCACAGTCTCCCCCTTCACCTGAACTT	4291
Qy	561	ThrSerGluGluAsnLysIleProAspAlaAspLysAlaAsnGluLysLysValAspGln	580
Db	4292	ACCTCAGAAGAAAAACAAAATCCAGATGCTGACAAAGCAAATGAAAAAAAAGTTGACCAG	4351
Qy	581	ProProGluAlaLysLysProLysIleLysValValAsnValGluLeuProIleGluAla	600
Db	4352	CCTCCAGAAGCTAAAAAGCCCCAAAATAAAGGTGGTGAATGTTGAGCTGCCTATTGAAGCC	4411
Qy	601	AsnLeuValTrpGlnLeuGlyLysAspLeuLeuAsnMetTyrIleGluThrGluGlyLys	620
Db	4412	AACTTGGTCTGGCAGTTAGGGAAAGACCTTCTTAACATGTATATTGAGACAGAGGGTAAG	4471
Qy	621	MetIleMetGlnAspLysLeuGluLysGluArgAsnAspAlaLysAsnAlaValGluGlu	640
Db	4472	ATGATAATGCAAGATAAATTGGAAAAAGAAAGGAATGATGTAAAAATGCAGTTGAGGAA	4531
Qy	641	TyrValTyrGluPheArgAspLysLeuCysGlyProTyrGluLysPheIleCysGluGln	660
Db	4532	TATGTGTATGAGTTTCAGAGACAAGCTGTGTGGACCATATGAAAAATTTATATGTGAGCAG	4591
Qy	661	AspHisGlnAsnPheLeuArgLeuLeuThrGluThrGluAspTrpLeuTyrGluGluGly	680
Db	4592	GATCATCAAAATTTTTTGAGACTCCTCACAGAACTGAAGACTGGCTGTATGAAGAAGGA	4651
Qy	681	GluAspGlnAlaLysGlnAlaTyrValAspLysLeuGluGluLeuMetLysIleGlyThr	700
Db	4652	GAGGACCAAGCTAAACAAGCATATGTTGACAAGTTGGAAGAATTATGAAAATTGGCACT	4711
Qy	701	ProValLysValArgPheGlnGluAlaGluGluArgProLysMetPheGluGluLeuGly	720
Db	4712	CCAGTTAAAGTTCGGTTTCAGGAAGCTGAAGAACGGCCAAAATGTTTGAAGAAGCTAGGA	4771
Qy	721	GlnArgLeuGlnHisTyrAlaLysIleAlaAlaAspPheArgAsnLysAspGluLysTyr	740
Db	4772	CAGAGGCTGCAGCATTATGCCAAGATAGCAGCTGACTTCAGAAATAAGGATGAGAAATAC	4831
Qy	741	AsnHisIleAspGluSerGluMetLysLysValGluLysSerValAsnGluValMetGlu	760

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      |||
Db      4832 AACCATATTGATGAGTCTGAAATGAAAAAGTGGAGAAGTCTGTTAATGAAGTGATGGAA 4891
Qy      761 TrpMetAsnAsnValMetAsnAlaGlnAlaLysLysSerLeuAspGlnAspProValVal 780
      |||
Db      4892 TGGATGAATAATGTCATGAATGCTCAGGCTAAAAAGAGTCTTGATCAGGATCCAGTTGTA 4951
Qy      781 ArgAlaGlnGluIleLysThrLysIleLysGluLeuAsnAsnThrCysGluProValVal 800
      |||
Db      4952 CGTGCTCAGGAAATTAAACAAAAATCAAGGAATTGAACAACACATGTGAACCCGTTGTA 5011
Qy      801 ThrGlnProLysProLysIleGluSerProLysLeuGluArgThrProAsnGlyProAsn 820
      |||
Db      5012 ACACAACCGAAACCAAAATTGAATCACCCAACTGGAAAGAACTCCAAATGGCCCAAAT 5071
Qy      821 IleAspLysLysGluGluAspLeuGluAspLysAsnAsnPheGlyAlaGluProProHis 840
      |||
Db      5072 ATTGATAAAAAGGAAGAAGATTTAGAAGACAAAAACAATTTTGGTGCTGAACCTCCACAT 5131
Qy      841 GlnAsnGlyGluCysTyrProAsnGluLysAsnSerValAsnMetAspLeuAsp 858
      |||
Db      5132 CAGAATGGTGAATGTTACCCTAATGAGAAAAATTCTGTTAATATGGACTTGGAC 5185

```

Scanlan teaches the use of the nucleic acids as probes (see column 8, lines 25-46) and also teaches the use of nucleic acids in expression vectors for therapeutic applications (see column 10, lines 8-16). Therefore, Scanlan teaches nucleic acids that are the same as that claimed.

8. Claims 9, 10, 21, 23, 24 and 26 are rejected under 35 U.S.C. 102(b) as being anticipated by Scanlan-II (Scanlan, M.J. et al., Int. J. Cancer 76: 652-658, 1998; cited in the IDS).

Scanlan-II teaches a nucleic acid, designated NY-CO-25, with GenBank accession no. AF039695) isolated from colon cancer samples and encoding a protein having similarity to hsp-110 (see page 653, Table 1A). Therefore, Scanlan-II teaches a nucleic acid that is the same as that claimed.

```

RESULT 3
AF039695
LOCUS      AF039695                3309 bp    mRNA    linear    PRI 05-MAY-1999
DEFINITION Homo sapiens antigen NY-CO-25 (NY-CO-25) mRNA, partial cds.
ACCESSION  AF039695
VERSION    AF039695.1  GI:3170189
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

```

Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3309)
AUTHORS Scanlan,M.J., Chen,Y.T., Williamson,B., Gure,A.O., Stockert,E.,
Gordan,J.D., Tureci,O., Sahin,U., Pfreundschuh,M. and Old,L.J.
TITLE Characterization of human colon cancer antigens recognized by
autologous antibodies
JOURNAL Int. J. Cancer 76 (5), 652-658 (1998)
PUBMED 9610721

REFERENCE 2 (bases 1 to 3309)
AUTHORS Scanlan,M.J.
TITLE Direct Submission
JOURNAL Submitted (23-DEC-1997) Ludwig Institute for Cancer Research, New
York Branch at Memorial Sloan-Kettering Cancer Center, 1275 York
Avenue, New York, NY 10021, USA

FEATURES Location/Qualifiers
source 1. .3309
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="colorectal carcinoma"
gene <1. .3309
/gene="NY-CO-25"
CDS <1. .2619
/gene="NY-CO-25"
/note="similar to hsp110 family members"
/codon_start=1
/product="antigen NY-CO-25"
/protein_id="AAC18044.1"
/db_xref="GI:3170190"
/translation="RRPRPEAEADREPAMSVVGLDVGSQSCYIAVARAGGIETIANEF
SDRCTPSVISFGSKNRTIGVAAKNQQITHANNTVSNFKRFHGRAFNDFPIQKEKENLS
YDLVPLKNGGVGIKVMYMGEEHLFSVEQITAMLLTKLKETAENSLKKPVTDCVISVPS
FFTDERRSVLDAAQIVGLNCLRLMNDMTAVALNYGIYKQDLPSLDEKPRIVVFVDMG
HSAFQVSACAFNKGKLVLTAFDPFLGGKNFDEKLVEHFCAEFKTKYKLDKSKIRA
LLRLYQCEKLLKLMSSNSTDLPLNIECFMNDKDVSGKMNRSQFEELCAELLQKIEVP
LYSLLEQTHLKVEDVSAVEIVGGATRIPAVKERIAKFFGKDIISTLNADAEAVARGCAL
QCAILSPAFAKVPREFSVTDVFPFISLIWNHDSDETEGVHEVFSRNHAAPFSKVLTFRLR
RGPFLEAFYSDDPQGVYPYPAKIGRFVVQNVSAQKDGEKSRVKKVVRVNTHGIFTIST
ASMVEKVPTEENEMSSEADMECLNQRPPENPDTDKNVQQDNSEAGTQPQVQTDAAQTS
QSPSPPELTSEENKIPDADKANEEKVDQPPEAKPKIKVNVNELPIEANLVWQLGKDL
LNMYIETEGKMIMQDKLEKERNDAKNAVEEYVYEFKDLKCGPYEKFICEQDHQNLRL
LTETEDWLYEEGEDQAKQAYVDKLEELMKIGTPVKVRFQEAERPKMFEELGQRLQHY
AKIAADFRNKDEKYNHIDSEMKKVEKSVNEVMEWMNNVMNAQAKKSLDQDPVVRQAE
IKTKIKELNNTCEPVVTQPKKIESPKLERTPNGPNIDKKEEDLEDKNNFGAEPHQN
GECYPNEKNSVNMDDL"

ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	3309
Score:	4450.00	Matches:	858
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-525-831-1 (1-858) x AF039695 (1-3309)

Qy 1 MetSerValValGlyLeuAspValGlySerGlnSerCysTyrIleAlaValAlaArgAla 20
|||||

Db 43 ATGTCGGTGGTGGGGTTGGACGTGGGCTCGCAGAGCTGCTACATCGCGGTAGCCCGGGCC 102

Qy 21 GlyGlyIleGluThrIleAlaAsnGluPheSerAspArgCysThrProSerValIleSer 40
|||||

Db 103 GGGGGCATCGAGACCATCGCAATGAGTTACGCGACCGGTGCACCCCGTCAGTCATATCA 162

Qy 41 PheGlySerLysAsnArgThrIleGlyValAlaAlaLysAsnGlnGlnIleThrHisAla 60

```

Db      163  |||||
Qy      61  AsnAsnThrValSerAsnPheLysArgPheHisGlyArgAlaPheAsnAspProPheIle 80
Db      223  |||||
Qy      81  GlnLysGluLysGluAsnLeuSerTyrAspLeuValProLeuLysAsnGlyGlyValGly 100
Db      283  |||||
Qy      101  IleLysValMetTyrMetGlyGluGluHisLeuPheSerValGluGlnIleThrAlaMet 120
Db      343  |||||
Qy      121  LeuLeuThrLysLeuLysGluThrAlaGluAsnSerLeuLysLysProValThrAspCys 140
Db      403  |||||
Qy      141  ValIleSerValProSerPhePheThrAspAlaGluArgArgSerValLeuAspAlaAla 160
Db      463  |||||
Qy      161  GlnIleValGlyLeuAsnCysLeuArgLeuMetAsnAspMetThrAlaValAlaLeuAsn 180
Db      523  |||||
Qy      181  TyrGlyIleTyrLysGlnAspLeuProSerLeuAspGluLysProArgIleValValPhe 200
Db      583  |||||
Qy      201  ValAspMetGlyHisSerAlaPheGlnValSerAlaCysAlaPheAsnLysGlyLysLeu 220
Db      643  |||||
Qy      221  LysValLeuGlyThrAlaPheAspProPheLeuGlyGlyLysAsnPheAspGluLysLeu 240
Db      703  |||||
Qy      241  ValGluHisPheCysAlaGluPheLysThrLysTyrLysLeuAspAlaLysSerLysIle 260
Db      763  |||||
Qy      261  ArgAlaLeuLeuArgLeuTyrGlnGluCysGluLysLeuLysLysLeuMetSerSerAsn 280
Db      823  |||||
Qy      281  SerThrAspLeuProLeuAsnIleGluCysPheMetAsnAspLysAspValSerGlyLys 300
Db      883  |||||
Qy      301  MetAsnArgSerGlnPheGluGluLeuCysAlaGluLeuLeuGlnLysIleGluValPro 320
Db      943  |||||
Qy      321  LeuTyrSerLeuLeuGluGlnThrHisLeuLysValGluAspValSerAlaValGluIle 340
Db      1003  |||||
Qy      341  ValGlyGlyAlaThrArgIleProAlaValLysGluArgIleAlaLysPhePheGlyLys 360
Db      1063  |||||
Qy      361  AspIleSerThrThrLeuAsnAlaAspGluAlaValAlaArgGlyCysAlaLeuGlnCys 380
Db      1123  |||||
```

Qy	381	AlaIleLeuSerProAlaPheLysValArgGluPheSerValThrAspAlaValProPhe	400
Db	1183	LeuSerProAlaPheLysValArgGluPheSerValThrAspAlaValProPhe GCAATACTTTCCCCGGCATTTAAAGTTAGAGAATTTTCCGTCACAGATGCAGTTCCCTTTT	1242
Qy	401	ProIleSerLeuIleTrpAsnHisAspSerGluAspThrGluGlyValHisGluValPhe	420
Db	1243	ProIleSerLeuIleTrpAsnHisAspSerGluAspThrGluGlyValHisGluValPhe CCAATATCTCTGATCTGGAACCATGATTTCAGAAGATACTGAAGGTGTTTCATGAAGTCTTT	1302
Qy	421	SerArgAsnHisAlaAlaProPheSerLysValLeuThrPheLeuArgArgGlyProPhe	440
Db	1303	SerArgAsnHisAlaAlaProPheSerLysValLeuThrPheLeuArgArgGlyProPhe AGTCGAAACCATGCTGCTCCTTTCTCCAAGTTCTCACCTTTCTGAGAAGGGGGCCTTTT	1362
Qy	441	GluLeuGluAlaPheTyrSerAspProGlnGlyValProTyrProGluAlaLysIleGly	460
Db	1363	GluLeuGluAlaPheTyrSerAspProGlnGlyValProTyrProGluAlaLysIleGly GAGCTAGAAGCTTTCTATTCTGATCCCCAAGGAGTTCATATCCAGAAGCAAAAATAGGC	1422
Qy	461	ArgPheValValGlnAsnValSerAlaGlnLysAspGlyGluLysSerArgValLysVal	480
Db	1423	ArgPheValValGlnAsnValSerAlaGlnLysAspGlyGluLysSerArgValLysVal CGCTTTGTAGTTTCTGATGTTTCTGTCACAGAAAGATGGAGAAAAATCTAGAGTAAAAGTC	1482
Qy	481	LysValArgValAsnThrHisGlyIlePheThrIleSerThrAlaSerMetValGluLys	500
Db	1483	LysValArgValAsnThrHisGlyIlePheThrIleSerThrAlaSerMetValGluLys AAAGTCGAGTCAACCCCATGGCATTTTCACCATCTCTACGGCATCTATGGTGGAGAAA	1542
Qy	501	ValProThrGluGluAsnGluMetSerSerGluAlaAspMetGluCysLeuAsnGlnArg	520
Db	1543	ValProThrGluGluAsnGluMetSerSerGluAlaAspMetGluCysLeuAsnGlnArg GTCCCAACTGAGGAGAATGAAATGTCTTCTGAAGCTGACATGGAGTGTCTGAATCAGAGA	1602
Qy	521	ProProGluAsnProAspThrAspLysAsnValGlnGlnAspAsnSerGluAlaGlyThr	540
Db	1603	ProProGluAsnProAspThrAspLysAsnValGlnGlnAspAsnSerGluAlaGlyThr CCACCAGAAAACCCAGACACTGATAAAAATGTCCAGCAAGACAACAGTGAAGCTGGAACA	1662
Qy	541	GlnProGlnValGlnThrAspAlaGlnGlnThrSerGlnSerProProSerProGluLeu	560
Db	1663	GlnProGlnValGlnThrAspAlaGlnGlnThrSerGlnSerProProSerProGluLeu CAGCCCCAGGTACAAACTGATGCTCAACAAACCTCACAGTCTCCCCCTTCACTGAACTT	1722
Qy	561	ThrSerGluGluAsnLysIleProAspAlaAspLysAlaAsnGluLysLysValAspGln	580
Db	1723	ThrSerGluGluAsnLysIleProAspAlaAspLysAlaAsnGluLysLysValAspGln ACCTCAGAAGAAAAACAAATCCCAGATGCTGACAAAGCAAAATGAAAAAAAAGTTGACCAG	1782
Qy	581	ProProGluAlaLysLysProLysIleLysValValAsnValGluLeuProIleGluAla	600
Db	1783	ProProGluAlaLysLysProLysIleLysValValAsnValGluLeuProIleGluAla CCTCCAGAAGCTAAAAAGCCCAAAATAAAGGTGGTGAATGTTGAGCTGCCTATTGAAGCC	1842
Qy	601	AsnLeuValTrpGlnLeuGlyLysAspLeuLeuAsnMetTyrIleGluThrGluGlyLys	620
Db	1843	AsnLeuValTrpGlnLeuGlyLysAspLeuLeuAsnMetTyrIleGluThrGluGlyLys AACTTGGTCTGGCAGTTAGGGAAAGACCTTCTTAACATGTATATTGAGACAGAGGGTAAG	1902
Qy	621	MetIleMetGlnAspLysLeuGluLysGluArgAsnAspAlaLysAsnAlaValGluGlu	640
Db	1903	MetIleMetGlnAspLysLeuGluLysGluArgAsnAspAlaLysAsnAlaValGluGlu ATGATAATGCAAGATAAATTGAAAAAGAAAGGAATGATGCTAAAAATGCAGTTGAGGAA	1962
Qy	641	TyrValTyrGluPheArgAspLysLeuCysGlyProTyrGluLysPheIleCysGluGln	660
Db	1963	TyrValTyrGluPheArgAspLysLeuCysGlyProTyrGluLysPheIleCysGluGln TATGTGTATGAGTTTCTGAGACAAAGCTGTGTGGACCATATGAAAAATTTATATGTGAGCAG	2022
Qy	661	AspHisGlnAsnPheLeuArgLeuLeuThrGluThrGluAspTrpLeuTyrGluGluGly	680
Db	2023	AspHisGlnAsnPheLeuArgLeuLeuThrGluThrGluAspTrpLeuTyrGluGluGly GATCATCAAAATTTTTTGAGACTCCTCACAGAACTGAAGACTGGCTGTATGAAGAAGGA	2082
Qy	681	GluAspGlnAlaLysGlnAlaTyrValAspLysLeuGluGluLeuMetLysIleGlyThr	700
Db	2083	GluAspGlnAlaLysGlnAlaTyrValAspLysLeuGluGluLeuMetLysIleGlyThr GAGGACCAAGCTAAACAAGCATATGTTGACAAGTTGGAAGAATTAATGAAAATTGGCACT	2142
Qy	701	ProValLysValArgPheGlnGluAlaGluGluArgProLysMetPheGluGluLeuGly	720


```

Db      2143  |||||
Qy      721  GlnArgLeuGlnHisTyrAlaLysIleAlaAlaAspPheArgAsnLysAspGluLysTyr 740
Db      2203  |||||
Qy      741  AsnHisIleAspGluSerGluMetLysLysValGluLysSerValAsnGluValMetGlu 760
Db      2263  |||||
Qy      761  TrpMetAsnAsnValMetAsnAlaGlnAlaLysLysSerLeuAspGlnAspProValVal 780
Db      2323  |||||
Qy      781  ArgAlaGlnGluIleLysThrLysIleLysGluLeuAsnAsnThrCysGluProValVal 800
Db      2383  |||||
Qy      801  ThrGlnProLysProLysIleGluSerProLysLeuGluArgThrProAsnGlyProAsn 820
Db      2443  |||||
Qy      821  IleAspLysLysGluGluAspLeuGluAspLysAsnAsnPheGlyAlaGluProProHis 840
Db      2503  |||||
Qy      841  GlnAsnGlyGluCysTyrProAsnGluLysAsnSerValAsnMetAspLeuAsp 858
Db      2563  |||||

```

9. Claims 9, 10, 21, 23, 24, and 26 are rejected under 35 U.S.C. 102(b) as being anticipated by Nakatsura (Biochemical and Biophysical Research Communications, 281: 936-944, 2001; cited in IDS) or Ishihara (Ishihara, K. et al. Biochem. Biophys. Acta, 1444: 138-142, 1999).

Nakatsura teaches a nucleic acid sequence that encodes a human hsp105 and teaches probes for use in detecting expression of hsp105 mRNA (see page 937, 1st paragraph, and also Figure 1). Ishihara teaches a nucleic acid sequence that encodes a human hsp105 protein (see legend to Figure 2 on page 139 and see below, alignment of SEQ ID NO: 1 with encoding nucleic acid sequence):

```

RESULT 1
HS105_HUMAN
ID   HS105_HUMAN      STANDARD;          PRT;   858 AA.
AC   Q92598; O95739; Q5TBM6; Q5TBM8; Q9UPC4;
DT   01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1997, sequence version 1.
DT   13-JUN-2006, entry version 63.
DE   Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antigen NY-

```

DE CO-25).

GN Name=HSPH1; Synonyms=HSP105, HSP110, KIAA0201;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

OC Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS ALPHA AND BETA), AND SUBCELLULAR

RP LOCATION.

RX MEDLINE=99132026; PubMed=9931472; DOI=10.1016/S0167-4781(98)00254-1;

RA Ishihara K., Yasuda K., Hatayama T.;

RT "Molecular cloning, expression and localization of human 105 kDa heat

RT shock protein, hsp105.";

RL Biochim. Biophys. Acta 1444:138-142(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM ALPHA).

RC TISSUE=Colon carcinoma;

RX MEDLINE=98272252; PubMed=9610721;

RX DOI=10.1002/(SICI)1097-0215(19980529)76:5<652::AID-IJC7>3.0.CO;2-P;

RA Scanlan M.J., Chen Y.-T., Williamson B., Gure A.O., Stockert E.,

RA Gordan J.D., Tuereci O., Sahin U., Pfreundschuh M., Old L.J.;

RT "Characterization of human colon cancer antigens recognized by

RT autologous antibodies.";

RL Int. J. Cancer 76:652-658(1998).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).

RC TISSUE=Bone marrow;

RX MEDLINE=97191544; PubMed=9039502; DOI=10.1093/dnares/3.5.321;

RA Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O.,

RA Tanaka A., Kotani H., Miyajima N., Nomura N.;

RT "Prediction of the coding sequences of unidentified human genes. VI.

RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by

RT analysis of cDNA clones from cell line KG-1 and brain.";

RL DNA Res. 3:321-329(1996).

RN [4]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PubMed=15057823; DOI=10.1038/nature02379;

RA Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,

RA Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E.,

RA Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E.,

RA Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,

RA Ashwell R.I.S., Babbage A.K., Baggeley C.L., Bailey J., Bannerjee R.,

RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,

RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clee C.M.,

RA Clegg S.C., Copley V., Collins J.E., Corby N., Coville G.J.,

RA Deloukas P., Dhami P., Dunham I., Dunn M., Earthworm M.E.,

RA Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,

RA Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,

RA Grafham D.V., Gribble S.M., Griffiths C., Hall R.E., Hammond S.,

RA Harley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,

RA Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,

RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,

RA Lloyd D.M., Lloyd C., Loveland J.E., Lovell J., Martin S.,

RA Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,

RA Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,

RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,

RA Sehra H.K., Shownkeen R., Skuce C.D., Smith M., Steward C.A.,

RA Sycamore N., Tester J., Thomas D.W., Tracey A., Tromans A., Tubby B.,

RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,

RA Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,

RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.;

RT "The DNA sequence and analysis of human chromosome 13.";

RL Nature 428:522-528(2004).

RN [5]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP TISSUE SPECIFICITY.
RX PubMed=10865058; DOI=10.1016/S0006-8993(00)02346-5;
RA Hylander B.L., Chen X., Graf P.C.F., Subjeck J.R.;
RT "The distribution and localization of hsp110 in brain.";
RL Brain Res. 869:49-55(2000).
RN [7]
RP TISSUE SPECIFICITY.
RX PubMed=16232202; DOI=10.1111/j.1349-7006.2005.00093.x;
RA Miyazaki M., Nakatsura T., Yokomine K., Senju S., Monji M., Hosaka S.,
RA Komori H., Yoshitake Y., Motomura Y., Minohara M., Kubo T.,
RA Ishihara K., Hatayama T., Ogawa M., Nishimura Y.;
RT "DNA vaccination of HSP105 leads to tumor rejection of colorectal
RT cancer and melanoma in mice through activation of both CD4 T cells and
RT CD8 T cells.";
RL Cancer Sci. 96:695-705(2005).
CC -!- FUNCTION: Prevents the aggregation of denatured proteins in cells
CC under severe stress, on which the ATP levels decrease markedly.
CC Inhibits HSPA8/HSC70 ATPase and chaperone activities (By
CC similarity).
CC -!- SUBUNIT: Interacts with HSPA8/HSC70 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasm.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=Q92598-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=Q92598-2; Sequence=VSP_002428;
CC -!- TISSUE SPECIFICITY: Highly expressed in testis. Present at lower
CC levels in most brain regions, except cerebellum. Overexpressed in
CC cancer cells.
CC -!- PTM: Phosphorylation on Ser-509 may be important for regulation of
CC the HSPA8/HSC70 chaperone activity (By similarity).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB003333; BAA34779.1; -; mRNA.
DR EMBL; AB003334; BAA34780.1; -; mRNA.
DR EMBL; AF039695; AAC18044.1; ALT_INIT; mRNA.
DR EMBL; D86956; BAA13192.2; ALT_INIT; mRNA.
DR EMBL; AL137142; CAI12428.1; -; Genomic_DNA.

DR EMBL; AL137142; CAI12430.1; -; Genomic_DNA.
DR EMBL; BC037553; AAH37553.1; -; mRNA.
DR UniGene; Hs.36927; -.
DR HSSP; P19120; 1BUP.
DR IntAct; Q92598; -.
DR Ensembl; ENSG00000120694; Homo sapiens.
DR H-InvDB; HIX0011215; -.
DR HGNC; HGNC:16969; HSPH1.
DR RZPD-ProtExp; I0011; -.
DR RZPD-ProtExp; I0298; -.
DR RZPD-ProtExp; IOH27526; -.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0006986; P:response to unfolded protein; TAS.
DR InterPro; IPR001023; Hsp70.
DR InterPro; IPR013126; Hsp_70.
DR PANTHER; PTHR19375; Hsp70; 2.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; FALSE_NEG.
DR PROSITE; PS00329; HSP70_2; FALSE_NEG.
DR PROSITE; PS01036; HSP70_3; 1.
KW Alternative splicing; ATP-binding; Heat shock; Nucleotide-binding;
KW Phosphorylation.
FT CHAIN 1 858 Heat-shock protein 105 kDa.
FT /FTid=PRO_0000078284.
FT MOD_RES 509 509 Phosphoserine (By similarity).
FT MOD_RES 557 557 Phosphoserine (By similarity).
FT MOD_RES 809 809 Phosphoserine (By similarity).
FT VAR_SEQ 529 572 Missing (in isoform Beta).
FT /FTid=VSP_002428.
SQ SEQUENCE 858 AA; 96865 MW; D0E757970E340B56 CRC64;

Query Match 100.0%; Score 4450; DB 1; Length 858;
Best Local Similarity 100.0%; Pred. No. 8.5e-205;
Matches 858; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSVVGLDVGVSQSCYIAVARAGGIETIANEFSDRCTPSVISFGSKNRTIGVAAKNQQITHA 60
|
Db 1 MSVVGLDVGVSQSCYIAVARAGGIETIANEFSDRCTPSVISFGSKNRTIGVAAKNQQITHA 60

Qy 61 NNTVSNFKRFHGRAFNDFPIQKEKENLSYDLVPLKNGGVGIKVMYMGEEHLFSVEQITAM 120
|
Db 61 NNTVSNFKRFHGRAFNDFPIQKEKENLSYDLVPLKNGGVGIKVMYMGEEHLFSVEQITAM 120

Qy 121 LLTKLKETAENSLKKPVTDCVISVPSFFTDARRSVLDAAQIVGLNCLRLMNDMTAVALN 180
|
Db 121 LLTKLKETAENSLKKPVTDCVISVPSFFTDARRSVLDAAQIVGLNCLRLMNDMTAVALN 180

Qy 181 YGIYKQDLPSLDEKPRIVVFVDMGHSAFQVSACAFNKGKLVLTAFDPFLGGKNFDEKL 240
|
Db 181 YGIYKQDLPSLDEKPRIVVFVDMGHSAFQVSACAFNKGKLVLTAFDPFLGGKNFDEKL 240

Qy 241 VEHFCAEFKTKYKLDASKIRALLRLYQCEKLLKLMSSNSTDLPLNIECFMNDKDVSGK 300
|
Db 241 VEHFCAEFKTKYKLDASKIRALLRLYQCEKLLKLMSSNSTDLPLNIECFMNDKDVSGK 300

Qy 301 MNRSQFEELCAELLQKIEVPLYSLLEQTHLKVEDVSAVEIVGGATRIPAVKERIAKFFGK 360
|
Db 301 MNRSQFEELCAELLQKIEVPLYSLLEQTHLKVEDVSAVEIVGGATRIPAVKERIAKFFGK 360

Qy 361 DISTTLNADEAVARGCALQCAILSPAFKVREFSVTDVAVFPISLIWNHDSDETEGVHEVF 420
|
Db 361 DISTTLNADEAVARGCALQCAILSPAFKVREFSVTDVAVFPISLIWNHDSDETEGVHEVF 420

Qy 421 SRNHAAPFSKVLTLFRRGPFLEAFYSDPQGVPEAKIGRFVVQNVSAQKDGEKSRVKV 480

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      |||
Db      421 SRNHAAPFSKVLTFLLRRGPFLEAFYSDPQGVPYPEAKIGRFVQNVSAQKDGEKSRVKV 480
Qy      481 KVRVNTHGIFTISTASMVEKVPTEENEMSSEADMECLNQRPPENPDTDKNVQQDNSEAGT 540
      |||
Db      481 KVRVNTHGIFTISTASMVEKVPTEENEMSSEADMECLNQRPPENPDTDKNVQQDNSEAGT 540
Qy      541 QPQVQTDAQQTSQSPSPPELTSEENKIPDADKANekkVDQPPEAKKPKIKVVNVELPIEA 600
      |||
Db      541 QPQVQTDAQQTSQSPSPPELTSEENKIPDADKANekkVDQPPEAKKPKIKVVNVELPIEA 600
Qy      601 NLVWQLGKDLLNMYIETEGKMIMQDKLEKERNDAKNAVEEYVVEFRDKLCGPYEKFICEQ 660
      |||
Db      601 NLVWQLGKDLLNMYIETEGKMIMQDKLEKERNDAKNAVEEYVVEFRDKLCGPYEKFICEQ 660
Qy      661 DHQNFLRLLTETEDWLYEEGEDQAKQAYVDKLEELMKIGTPVKVRFQAEERPCKMFEELG 720
      |||
Db      661 DHQNFLRLLTETEDWLYEEGEDQAKQAYVDKLEELMKIGTPVKVRFQAEERPCKMFEELG 720
Qy      721 QRLQHYAKIAADFRNKDEKYNHIDSEMKKVEKSVNEVMEWMNNVMNAQAKKSLDQDPVV 780
      |||
Db      721 QRLQHYAKIAADFRNKDEKYNHIDSEMKKVEKSVNEVMEWMNNVMNAQAKKSLDQDPVV 780
Qy      781 RAQEIKTKIKELNNTCEPVVTQPKPKIESPKLERTPNGPNIDKKEEDLEDKNNFGAEP PH 840
      |||
Db      781 RAQEIKTKIKELNNTCEPVVTQPKPKIESPKLERTPNGPNIDKKEEDLEDKNNFGAEP PH 840
Qy      841 QNGECYPNEKNSVNMDLD 858
      |||
Db      841 QNGECYPNEKNSVNMDLD 858

```

Therefore, either Nakatsura or Ishihara teaches a nucleic acid that is the same as that claimed.

10. Claims 9, 10, 21, 23, 24 and 26 are rejected under 35 U.S.C. 102(e) as being anticipated by Horne (US 6,974,667; issued 12/13/2005; effective filing date is Jun. 14, 2001), Kaser (US 6,727,006; issued 4/27/2004; effective filing date is Jul. 30, 2001), or Cocks (US. 6,607,879; issued Au. 19, 2003; effective filing date is Feb. 9, 1998).

Horne, Kaser or Cocks teaches a nucleic acid sequence that encodes a polypeptide comprising the amino acid sequence of SEQ ID NO: 1. Horne, Kaser or Cocks also inherently teach nucleic acids that are the complete complements of their disclosed sequences and therefore, teach a nucleic acid sequence that would hybridize to a DNA having the nucleotide sequence shown in SEQ ID NO: 2 under stringent conditions, because their nucleic acids are have almost

100% identity with the sequence of SEQ ID NO: 2. Such a nucleic acid sequence would also be one that has (interpret as comprising) a partial sequence of SEQ ID NO: 2. Because claim 21 is drawn to a cancer vaccine which comprises a DNA of claim 9, the term "cancer vaccine" is interpreted as intended use because it does not appear to structurally affect the scope of a DNA of claim 9. Therefore, Horne, Kaser or Cocks teaches a cancer vaccine of claim 21. Horne, Kaser or Cocks teaches probes for diagnoses (see abstracts). Therefore, Horne, Kaser or Cocks teaches the claimed products. Alignments of SEQ ID NO: 2 with the sequences of Horne, Kaser or Cocks:

```
RESULT 1
US-09-919-039-176
; Sequence 176, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 176
; LENGTH: 4244
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 048488.32
US-09-919-039-176
```

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Query Match          99.3%; Score 3585.4; DB 3; Length 4244;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3608; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
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Qy      1 GAGGAAGTGGGACCTCCCCTTTTGGGTCGGTAGTTTACGCGCCGGCGCCGGTGTGCGAGCC 60
      |||
Db      3 GAGGAAGTGGGACCTCCCCTTTTGGGTCGGTAGTTTACGCGCCGGCGCCGGTGTGCGAGCC 62

Qy     61 GCGGCAGAGTGAGGCAGGCAACCCGAGGTGCGGAGCGACCTGCGGAGGCTGAGCCCCGCT 120
      |||
Db     63 GCGGCAGAGTGAGGCAGGCAACCCGAGGTGCGGAGCGACCTGCGGAGGCTGAGCCCCGCT 122

Qy    121 TTCTCCCAGGGTTTCTTATCAGCCAGCCGCCGCTGTCCCCGGGGGAGTAGGAGGCTCCTG 180
      |||
Db    123 TTCTCCCAGGGTTTCTTATCAGCCAGCCGCCGCTGTCCCCGGGGGAGTAGGAGGCTCCTG 182
```

Qy	181	ACAGGCCGCGGCTGTCTGTGTGTCCTTCTGAGTGTGTCAGAGGAACGGCCAGACCCCCGCGGG	240
Db	183	ACAGGCCGCGGCTGTCTGTGTGTCCTTCTGAGTGTGTCAGAGGAACGGCCAGACCCCCGCGGG	242
Qy	241	CCGGAGCAGAACGCGGCCAGGGCAGAAAGCGGCGGCAGGAGAAGCAGGCAGGGGGCCGGA	300
Db	243	CCGGAGCAGAACGCGGCCAGGGCAGAAAGCGGCGGCAGGAGAAGCAGGCAGGGGGCCGGA	302
Qy	301	GGACGCAGACCCGAGACCCGAGGCGGAGGCGGACCGCGAGCCGGCCATGTCGGTGGTGGGG	360
Db	303	GGACGCAGACCCGAGACCCGAGGCGGAGGCGGACCGCGAGCCGGCCATGTCGGTGGTGGGG	362
Qy	361	TTGGACGTGGGCTCGCAGAGCTGCTACATCGCGGTAGCCCGGGCCGGGGGCATCGAGACC	420
Db	363	TTGGACGTGGGCTCGCAGAGCTGCTACATCGCGGTAGCCCGGGCCGGGGGCATCGAGACC	422
Qy	421	ATCGCCAATGAGTTACAGCGACCGGTGCACCCCGTCAGTCATATCATTGATCAAAAAAT	480
Db	423	ATCGCCAATGAGTTACAGCGACCGGTGCACCCCGTCAGTCATATCATTGATCAAAAAAT	482
Qy	481	AGAACAATCGGAGTTGCGAGCCAAAAATCAGCAAATCACTCATGCAAAACAATACGGTGTCT	540
Db	483	AGAACAATCGGAGTTGCGAGCCAAAAATCAGCAAATCACTCATGCAAAACAATACGGTGTCT	542
Qy	541	AACTTCAAAAGATTTTCATGGCCGAGCATTCAACGACCCCTTCATTCAAAAGGAGAAGGAA	600
Db	543	AACTTCAAAAGATTTTCATGGCCGAGCATTCAACGACCCCTTCATTCAAAAGGAGAAGGAA	602
Qy	601	AACTTGAGTTACGATTGTTTCCATTGAAAAATGGTGGAGTTGGAATAAAGGTAATGTAC	660
Db	603	AACTTGAGTTACGATTGTTTCCATTGAAAAATGGTGGAGTTGGAATAAAGGTAATGTAC	662
Qy	661	ATGGGTGAAGAACATCTATTTAGTGTGGAGCAGATAACAGCCATGTTGTTGACTAAGCTG	720
Db	663	ATGGGTGAAGAACATCTATTTAGTGTGGAGCAGATAACAGCCATGTTGTTGACTAAGCTG	722
Qy	721	AAGGAAACTGCTGAAACAGCCTCAAGAAACAGTAACAGATTGTGTTATTTAGTCCCC	780
Db	723	AAGGAAACTGCTGAAACAGCCTCAAGAAACAGTAACAGATTGTGTTATTTAGTCCCC	782
Qy	781	TCCTTCTTTACAGATGCTGAGAGGCGATCTGTGTTAGATGCTGCACAGATTGTTGGCCTA	840
Db	783	TCCTTCTTTACAGATGCTGAGAGGCGATCTGTGTTAGATGCTGCACAGATTGTTGGCCTA	842
Qy	841	AACTGTTTAAGACTTATGAATGACATGACAGCTGTTGCTTTGAATTACGGAATTTATAAG	900
Db	843	AACTGTTTAAGACTTATGAATGACATGACAGCTGTTGCTTTGAATTACGGAATTTATAAG	902
Qy	901	CAGGATCTCCAAGCCTGGATGAGAAACCTCGGATAGTGGTTTTTGTGTGATATGGGACAT	960
Db	903	CAGGATCTCCAAGCCTGGATGAGAAACCTCGGATAGTGGTTTTTGTGTGATATGGGACAT	962
Qy	961	TCAGCTTTTCAAGTGTCTGCTTGTGCTTTTAAACAGGGAAAAATTGAAGGTACTGGGAACA	1020
Db	963	TCAGCTTTTCAAGTGTCTGCTTGTGCTTTTAAACAGGGAAAAATTGAAGGTACTGGGAACA	1022
Qy	1021	GCTTTTGATCCTTTCTTAGGAGGAAAAAACTTCGATGAAAAGTTAGTGGAACATTTCTGT	1080
Db	1023	GCTTTTGATCCTTTCTTAGGAGGAAAAAACTTCGATGAAAAGTTAGTGGAACATTTCTGT	1082
Qy	1081	GCAGAAATTTAAACTAAGTACAAGTTGGATGCAAAATCCAAAATACGAGCACTCCTACGT	1140
Db	1083	GCAGAAATTTAAACTAAGTACAAGTTGGATGCAAAATCCAAAATACGAGCACTCCTACGT	1142
Qy	1141	CTGTATCAGGAATGTGAAAAACTGAAAAAGCTAATGAGCTCTAACAGCACAGACCTTCCA	1200

Db 1143 CTGTATCAGGAATGTGAAAACTGAAAAAGCTAATGAGCTCTAACAGCACAGACCTTCCA 1202

Qy 1201 CTGAATATCGAATGCTTTATGAATGATAAAGATGTTTCCGAAAGATGAACAGGTCACAA 1260
|||||

Db 1203 CTGAATATCGAATGCTTTATGAATGATAAAGATGTTTCCGAAAGATGAACAGGTCACAA 1262

Qy 1261 TTTGAAGAACTCTGTGCTGAACCTTCTGCAAAAGATAGAAGTACCCCTTTATTCACTGTTG 1320
|||||

Db 1263 TTTGAAGAACTCTGTGCTGAACCTTCTGCAAAAGATAGAAGTACCCCTTTATTCACTGTTG 1322

Qy 1321 GAACAAACTCATCTCAAAGTAGAAGATGTGAGTGCAGTTGAGATTGTTGGAGGCGCTACA 1380
|||||

Db 1323 GAACAAACTCATCTCAAAGTAGAAGATGTGAGTGCAGTTGAGATTGTTGGAGGCGCTACA 1382

Qy 1381 CGAATTCCAGCTGTGAAGGAAAGAATTGCCAAATTCTTTGGAAAAGATATTAGCACACA 1440
|||||

Db 1383 CGAATTCCAGCTGTGAAGGAAAGAATTGCCAAATTCTTTGGAAAAGATATTAGCACACA 1442

Qy 1441 CTCAATGCAGATGAAGCAGTAGCCAGAGGATGTGCATTACAGTGTGCAATACTTTCCCG 1500
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Db 1443 CTCAATGCAGATGAAGCAGTAGCCAGAGGATGTGCATTACAGTGTGCAATACTTTCCCG 1502

Qy 1501 GCATTTAAAGTTAGAGAATTTTCCGTACAGATGCAGTTCCTTTCCAATATCTCTGATC 1560
|||||

Db 1503 GCATTTAAAGTTAGAGAATTTTCCGTACAGATGCAGTTCCTTTCCAATATCTCTGATC 1562

Qy 1561 TGAACCATGATTTCAGAAGATACTGAAGGTGTTTCATGAAGTCCTTAGTCGAAACCATGCT 1620
|||||

Db 1563 TGAACCATGATTTCAGAAGATACTGAAGGTGTTTCATGAAGTCCTTAGTCGAAACCATGCT 1622

Qy 1621 GCTCCTTTCTCAAAGTTCTCACCTTTCTGAGAAGGGGGCCTTTGAGCTAGAAGCTTTC 1680
|||||

Db 1623 GCTCCTTTCTCAAAGTTCTCACCTTTCTGAGAAGGGGGCCTTTGAGCTAGAAGCTTTC 1682

Qy 1681 TATTCTGATCCCCAAGGAGTTCATATCCAGAAGCAAAATAGGCCGCTTTGTAGTTCAG 1740
|||||

Db 1683 TATTCTGATCCCCAAGGAGTTCATATCCAGAAGCAAAATAGGCCGCTTTGTAGTTCAG 1742

Qy 1741 AATGTTTCTGCACAGAAAGATGGAGAAAAATCTAGAGTAAAAGTCAAAGTGCAGTCAAC 1800
|||||

Db 1743 AATGTTTCTGCACAGAAAGATGGAGAAAAATCTAGAGTAAAAGTCAAAGTGCAGTCAAC 1802

Qy 1801 ACCCATGGCATTTTACCATCTCTACGGCATCTATGGTGGAGAAAGTCCCAACTGAGGAG 1860
|||||

Db 1803 ACCCATGGCATTTTACCATCTCTACGGCATCTATGGTGGAGAAAGTCCCAACTGAGGAG 1862

Qy 1861 AATGAAATGTCTTCTGAAGCTGACATGGAGTGTCTGAATCAGAGACCACCAGAAAACCCA 1920
|||||

Db 1863 AATGAAATGTCTTCTGAAGCTGACATGGAGTGTCTGAATCAGAGACCACCAGAAAACCCA 1922

Qy 1921 GACACTGATAAAAAATGTCCAGCAAGACAACAGTGAAGCTGGAACACAGCCCCAGGTACAA 1980
|||||

Db 1923 GACACTGATAAAAAATGTCCAGCAAGACAACAGTGAAGCTGGAACACAGCCCCAGGTACAA 1982

Qy 1981 ACTGATGCTCAACAAACCTCACAGTCTCCCCCTTACCTGAACCTTACCTCAGAAGAAAAC 2040
|||||

Db 1983 ACTGATGCTCAACAAACCTCACAGTCTCCCCCTTACCTGAACCTTACCTCAGAAGAAAAC 2042

Qy 2041 AAAATCCAGATGCTGACAAAGCAAATGAAAAAAAAGTTGACCAGCCTCCAGAAGCTAAA 2100
|||||

Db 2043 AAAATCCAGATGCTGACAAAGCAAATGAAAAAAAAGTTGACCAGCCTCCAGAAGCTAAA 2102

Qy 2101 AAGCCCAAAATAAAGGTGGTGAATGTTGAGCTGCCTATTGAAGCCAACTTGGTCTGGCAG 2160
|||||

Db 2103 AAGCCCAAAATAAAGGTGGTGAATGTTGAGCTGCCTATTGAAGCCAACTTGGTCTGGCAG 2162

Qy	2161	TTAGGGAAAGACCTTCTTAACATGTATATTGAGACAGAGGGTAAGATGATAATGCAAGAT	2220
Db	2163	TTAGGGAAAGACCTTCTTAACATGTATATTGAGACAGAGGGTAAGATGATAATGCAAGAT	2222
Qy	2221	AAATTGGAAAAAGAAAGGAATGATGCTAAAAATGCAGTTGAGGAATATGTGTATGAGTTTC	2280
Db	2223	AAATTGGAAAAAGAAAGGAATGATGCTAAAAATGCAGTTGAGGAATATGTGTATGAGTTTC	2282
Qy	2281	AGAGACAAGCTGTGTGGACCATATGAAAAATTTATATGTGAGCAGGATCATCAAAATTTT	2340
Db	2283	AGAGACAAGCTGTGTGGACCATATGAAAAATTTATATGTGAGCAGGATCATCAAAATTTT	2342
Qy	2341	TTGAGACTCCTCACAGAAACTGAAGACTGGCTGTATGAAGAAGGAGAGGACCAAGCTAAA	2400
Db	2343	TTGAGACTCCTCACAGAAACTGAAGACTGGCTGTATGAAGAAGGAGAGGACCAAGCTAAA	2402
Qy	2401	CAAGCATATGTTGACAAGTTGGAAGAATTAATGAAAATTGGCACTCCAGTTAAAGTTCGG	2460
Db	2403	CAAGCATATGTTGACAAGTTGGAAGAATTAATGAAAATTGGCACTCCAGTTAAAGTTCGG	2462
Qy	2461	TTTCAGGAAGCTGAAGAACCGGCCAAAAATGTTTGAAGAACTAGGACAGAGGCTGCAGCAT	2520
Db	2463	TTTCAGGAAGCTGAAGAACCGGCCAAAAATGTTTGAAGAACTAGGACAGAGGCTGCAGCAT	2522
Qy	2521	TATGCCAAGATAGCAGCTGACTTCAGAAATAAGGATGAGAAATACAACCATATTGATGAG	2580
Db	2523	TATGCCAAGATAGCAGCTGACTTCAGAAATAAGGATGAGAAATACAACCATATTGATGAG	2582
Qy	2581	TCTGAAATGAAAAAAGTGGAGAAGTCTGTTAATGAAGTGATGGAATGGATGAATAATGTC	2640
Db	2583	TCTGAAATGAAAAAAGTGGAGAAGTCTGTTAATGAAGTGATGGAATGGATGAATAATGTC	2642
Qy	2641	ATGAATGCTCAGGCTAAAAAGAGTCTTGATCAGGATCCAGTTGTACGTGCTCAGGAAATT	2700
Db	2643	ATGAATGCTCAGGCTAAAAAGAGTCTTGATCAGGATCCAGTTGTACGTGCTCAGGAAATT	2702
Qy	2701	AAAACAAAAATCAAGGAATTGAACAACACATGTGAACCCGTTGTAACACAACCGAAACCA	2760
Db	2703	AAAACAAAAATCAAGGAATTGAACAACACATGTGAACCCGTTGTAACACAACCGAAACCA	2762
Qy	2761	AAAATTGAATCACCCAAACCTGGAAGAAGTCCAAATGGCCCAAATATTGATAAAAAGGAA	2820
Db	2763	AAAATTGAATCACCCAAACCTGGAAGAAGTCCAAATGGCCCAAATATTGATAAAAAGGAA	2822
Qy	2821	GAAGATTTAGAAGACAAAAACAATTTTGGTGCTGAACCTCCACATCAGAATGGTGAATGT	2880
Db	2823	GAAGATTTAGAAGACAAAAACAATTTTGGTGCTGAACCTCCACATCAGAATGGTGAATGT	2882
Qy	2881	TACCCTAATGAGAAAAATTCTGTTAATATGGACTTGGACTAGATAACCTTAAATTGGCCT	2940
Db	2883	TACCCTAATGAGAAAAATTCTGTTAATATGGACTTGGACTAGATAACCTTAAATTGGCCT	2942
Qy	2941	ATTCCITCAATTAAATAAAATAATTTTGGCCATAGTATGTGACTCTACATAACATACTGAAA	3000
Db	2943	ATTCCITCAATTAAATAAAATAATTTTGGCCATAGTATGTGACTCTACATAACATACTGAAA	3002
Qy	3001	CTATTTATATTTTCTTTTTTAAGGATATTTAGAAATTTTGTGTATTATATGGAAAAAGAA	3060
Db	3003	CTATTTATATTTTCTTTTTTAAGGATATTTAGAAATTTTGTGTATTATATGGAAAAAGAA	3062
Qy	3061	AAAAAGCTTAAGTCTGTAGTCTTTATGATCCTAAAAGGGAAAAATTGCCTTGGTAACTTTC	3120
Db	3063	AAAAAGCTTAAGTCTGTAGTCTTTATGATCCTAAAAGGGAAAAATTGCCTTGGTAACTTTC	3122
Qy	3121	AGATTCCCTGTGGAATTGTGAATTCATACTAAGCTTTTCTGTGCAGTCTCACCATTTCATC	3180

Application/Control Number:
10/525,831
Art Unit: 1643

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Db      3123 AGATTCTGTGGAATTGTGAATTCATACTAAGCTTTCTGTGCAGTCTCACCATTTCATC 3182

Qy      3181 ACTGAGGATGAAACTGACTTTTGTCTTTTGGAGAAAAAACTGTACTG-TTGTTCAGA 3239
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3183 ACTGAGGATGAAACTGACTTTTGTCTTTTGGAGAAAAAACTGTACTGCTTGTTCAGA 3242

Qy      3240 GGGCTGTGATTAAAATCTTTAAGCATTTGTTCTGCCAAGGTAGTTTCTTGCAATTTTGC 3299
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3243 GGGCTGTGATTAAAATCTTTAAGCATTTGTTCTGCCAAGGTAGTTTCTTGCAATTTTGC 3302

Qy      3300 TCTCCATTTCAGCATGTGTGTGGGTGTGGATGTTTATAACAAGACTAAGTCTGACTTCAT 3359
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3303 TCTCCATTTCAGCATGTGTGTGGGTGTGGATGTTTATAACAAGACTAAGTCTGACTTCAT 3362

Qy      3360 AAGGGCTTTCTAAAACCATTTCTGTCCAAGAGAAAATGACTTTTGTCTTTGATATTAAAA 3419
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3363 AAGGGCTTTCTAAAACCATTTCTGTCCAAGAGAAAATGACTTTTGTCTTTGATATTAAAA 3422

Qy      3420 ATTCAATGAGTAAAACAAAAGCTAGTCAAATGTGTTAGCAGCATGCAGAACAAAACTTT 3479
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3423 ATTCAATGAGTAAAACAAAAGCTAGTCAAATGTGTTAGCAGCATGCAGAACAAAACTTT 3482

Qy      3480 AAACCTTCTCTCTCACTATACAGTATATTGTCAATGTGAAAGTGTGGAATGGAAGAAATG 3539
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3483 AAACCTTCTCTCTCACTATACAGTATATTGTC-ATGTGAAAGTGTGGAATGGAAGAAATG 3541

Qy      3540 TCGATCCTGTTGTAAGTGAATGTAACACTTTTATGAGCTTTAAAATAAAGTTCATCTTA 3599
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3542 TCGATCCTGTTGTAAGTGAATGTAACACTTTTATGAGCTTTAAAATAAAGTTCATCTTA 3601

Qy      3600 TGGTGTCAATTT 3610
        |||||||||||
Db      3602 TGGTGTCAATTT 3612
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RESULT 2

US-09-023-655-968

; Sequence 968, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

Application/Control Number:
10/525,831
Art Unit: 1643

Page 26

; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 968:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3614 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1503985
US-09-023-655-968

Query Match 99.2%; Score 3583.8; DB 3; Length 3614;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3607; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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Qy      1 GAGGAAGTGGGACCTCCCTTTTGGGTCGGTAGTTTCAGCGCCGGCGCGGTGTGCGAGCC 60
          |||
Db      3 GAGGAAGTGGGACCTCCCTTTTGGGTCGGTAGTTTCAGCGCCGGCGCGGTGTGCGAGCC 62

Qy     61 GCGGCAGAGTGAGGCAGGCAACCCGAGGTGCGGAGCGACCTGCGGAGGCTGAGCCCCGCT 120
          |||
Db     63 GCGGCAGAGTGAGGCAGGCAACCCGAGGTGCGGAGCGACCTGCGGAGGCTGAGCCCCGCT 122

Qy    121 TTCTCCCAGGGTTTCTTATCAGCCAGCCGCGCTGTCCCCGGGGGAGTAGGAGGCTCCTG 180
          |||
Db    123 TTCTCCCAGGGTTTCTTATCAGCCAGCCGCGCTGTCCCCGGGGGAGTAGGAGGCTCCTG 182

Qy    181 ACAGGCCGCGGCTGTCTGTGTGTCCTTCTGAGTGTGTCAGAGGAACGGCCAGACCCGCGGG 240
          |||
Db    183 ACAGGCCGCGGCTGTCTGTGTGTCCTTCTGAGTGTGTCAGAGGAACGGCCAGACCCGCGGG 242

Qy    241 CCGGAGCAGAACCGCGCCAGGGCAGAAAGCGGCGGCAGGAGAAGCAGGCAGGGGGCCGGA 300
          |||
Db    243 CCGGAGCAGAACCGCGCCAGGGCAGAAAGCGGCGGCAGGAGAAGCAGGCAGGGGGCCGGA 302

Qy    301 GGACGCAGACCGAGACCCGAGGCGGAGGCGGACCGCGAGCCGGCCATGTCGGTGGTGGGG 360
          |||
Db    303 GGACGCAGACCGAGACCCGAGGCGGAGGCGGACCGCGAGCCGGCCATGTCGGTGGTGGGG 362

Qy    361 TTGGACGTGGGCTCGCAGAGCTGCTACATCGCGGTAGCCCGGGCCGGGGGCATCGAGACC 420
          |||
Db    363 TTGGACGTGGGCTCGCAGAGCTGCTACATCGCGGTAGCCCGGGCCGGGGGCATCGAGACC 422

Qy    421 ATCGCCAATGAGTTTCAGCGACCGGTGCACCCCGTCAGTCATATCATTGATCAAAAAAT 480
          |||
Db    423 ATCGCCAATGAGTTTCAGCGACCGGTGCACCCCGTCAGTCATATCATTGATCAAAAAAT 482

Qy    481 AGAACAATCGGAGTTGTCAGCCAAAAATCAGCAAATCACTCATGCAAACAATACGGTGTCT 540
          |||
Db    483 AGAACAATCGGAGTTGTCAGCCAAAAATCAGCAAATCACTCATGCAAACAATACGGTGTCT 542

Qy    541 AACTTCAAAAGATTTTCATGGCCGAGCATTCAACGACCCCTTCATTCAAAAGGAGAAGGAA 600
          |||
Db    543 AACTTCAAAAGATTTTCATGGCCGAGCATTCAATGACCCCTTCATTCAAAAGGAGAAGGAA 602

Qy    601 AACTTGAGTTACGATTGTTCCATTGAAAAATGGTGGAGTTGGAATAAAGTAATGTAC 660
          |||
Db    603 AACTTGAGTTACGATTGTTCCATTGAAAAATGGTGGAGTTGGAATAAAGTAATGTAC 662
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Qy	661	ATGGGTGAAGAACATCTATTTAGTGTGGAGCAGATAACAGCCATGTTGTTGACTAAGCTG	720
Db	663	ATGGGTGAAGAACATCTATTTAGTGTGGAGCAGATAACAGCCATGTTGTTGACTAAGCTG	722
Qy	721	AAGGAAACTGCTGAAAACAGCCTCAAGAAACCAGTAACAGATTGTGTTATTTTCAGTCCCC	780
Db	723	AAGGAAACTGCTGAAAACAGCCTCAAGAAACCAGTAACAGATTGTGTTATTTTCAGTCCCC	782
Qy	781	TCCTTCTTTACAGATGCTGAGAGGCGATCTGTGTTAGATGCTGCACAGATTGTTGGCCTA	840
Db	783	TCCTTCTTTACAGATGCTGAGAGGCGATCTGTGTTAGATGCTGCACAGATTGTTGGCCTA	842
Qy	841	AACTGTTTAAAGACTTATGAATGACATGACAGCTGTTGCTTTGAATTACGGAATTTATAAG	900
Db	843	AACTGTTTAAAGACTTATGAATGACATGACAGCTGTTGCTTTGAATTACGGAATTTATAAG	902
Qy	901	CAGGATCTCCCAAGCCTGGATGAGAAACCTCGGATAGTGGTTTTGTGATATGGGACAT	960
Db	903	CAGGATCTCCCAAGCCTGGATGAGAAACCTCGGATAGTGGTTTTGTGATATGGGACAT	962
Qy	961	TCAGCTTTTCAAGTGCTGCTTGTGCTTTTAAACAAGGGAATAATGAAGGTACTGGGAACA	1020
Db	963	TCAGCTTTTCAAGTGCTGCTTGTGCTTTTAAACAAGGGAATAATGAAGGTACTGGGAACA	1022
Qy	1021	GCTTTTGTATCCTTTCTTAGGAGGAAAAAACTTCGATGAAAAGTTAGTGGAAACATTTCTGT	1080
Db	1023	GCTTTTGTATCCTTTCTTAGGAGGAAAAAACTTCGATGAAAAGTTAGTGGAAACATTTTGT	1082
Qy	1081	GCAGAAATTTAAAACTAAGTACAAGTTGGATGCAAAATCCAAAATACGAGCACTCCTACGT	1140
Db	1083	GCAGAAATTTAAAACTAAGTACAAGTTGGATGCAAAATCCAAAATACGAGCACTCCTACGT	1142
Qy	1141	CTGTATCAGGAATGTGAAAACTGAAAAAGCTAATGAGCTCTAACAGCACAGACCTTCCA	1200
Db	1143	CTGTATCAGGAATGTGAAAACTGAAAAAGCTAATGAGCTCTAACAGCACAGACCTTCCA	1202
Qy	1201	CTGAATATCGAATGCTTTATGAATGATAAAGATGTTTCCGGAAGATGAACAGGTCACAA	1260
Db	1203	CTGAATATCGAATGCTTTATGAATGATAAAGATGTTTCCGGAAGATGAACAGGTCACAA	1262
Qy	1261	TTTGAAGAACTCTGTGCTGAACCTTCTGCAAAAGATAGAAGTACCCCTTTATTCACTGTG	1320
Db	1263	TTTGAAGAACTCTGTGCTGAACCTTCTGCAAAAGATAGAAGTACCCCTTTATTCACTGTG	1322
Qy	1321	GAACAAACTCATCTCAAAGTAGAAGATGTGAGTGCAGTTGAGATTGTTGGAGGCGCTACA	1380
Db	1323	GAACAAACTCATCTCAAAGTAGAAGATGTGAGTGCAGTTGAGATTGTTGGAGGCGCTACA	1382
Qy	1381	CGAATTCCAGCTGTGAAGGAAAGAAATGCCAAATTCCTTTGGAAAAGATATTAGCACAACA	1440
Db	1383	CGAATTCCAGCTGTGAAGGAAAGAAATGCCAAATTCCTTTGGAAAAGATATTAGCACAACA	1442
Qy	1441	CTCAATGCAGATGAAGCAGTAGCCAGAGGATGTGCATTACAGTGTGCAATACTTTCCCGG	1500
Db	1443	CTCAATGCAGATGAAGCAGTAGCCAGAGGATGTGCATTACAGTGTGCAATACTTTCCCGG	1502
Qy	1501	GCATTTAAAGTTAGAGAATTTTCCGTCACAGATGCAGTTCCTTTTCCAATATCTCTGATC	1560
Db	1503	GCATTTAAAGTTAGAGAATTTTCCGTCACAGATGCAGTTCCTTTTCCAATATCTCTGATC	1562
Qy	1561	TGGAACCATGATTGAGAAGATACTGAAGGTGTTTCATGAAGTCTTTAGTCGAAACCATGCT	1620
Db	1563	TGGAACCATGATTGAGAAGATACTGAAGGTGTTTCATGAAGTCTTTAGTCGAAACCATGCT	1622
Qy	1621	GCTCCTTTTCTCCAAAGTTCTCACCTTTCTGAGAAGGGGGCCTTTTGTGCTAGAAGCTTTT	1680

Db 1623 GCTCCTTTCTCCAAAGTTCTCACCTTTCTGAGAAGGGGGCCTTTTGAGCTAGAAGCTTTC 1682

Qy 1681 TATTCTGATCCCCAAGGAGTTCCATATCCAGAAGCAAAAATAGGCCGCTTTGTAGTTCAG 1740
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Db 1683 TATTCTGATCCCCAAGGAGTTCCATATCCAGAAGCAAAAATAGGCCGCTTTGTAGTTCAG 1742

Qy 1741 AATGTTTCTGCACAGAAAGATGGAGAAAAATCTAGAGTAAAAGTCAAAGTGCAGTCAAC 1800
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Db 1743 AATGTTTCTGCACAGAAAGATGGAGAAAAATCTAGAGTAAAAGTCAAAGTGCAGTCAAC 1802

Qy 1801 ACCCATGGCATTTTCACCATCTCTACGGCATCTATGGTGGAGAAAGTCCCAACTGAGGAG 1860
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Db 1803 ACCCATGGCATTTTCACCATCTCTACGGCATCTATGGTGGAGAAAGTCCCAACTGAGGAG 1862

Qy 1861 AATGAAATGTCTTCTGAAGCTGACATGGAGTGTCTGAATCAGAGACCACCAGAAAACCA 1920
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Db 1863 AATGAAATGTCTTCTGAAGCTGACATGGAGTGTCTGAATCAGAGACCACCAGAAAACCA 1922

Qy 1921 GACACTGATAAAAAATGTCCAGCAAGACAACAGTGAAGCTGGAACACAGCCCCAGGTACAA 1980
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Db 1923 GACACTGATAAAAAATGTCCAGCAAGACAACAGTGAAGCTGGAACACAGCCCCAGGTACAA 1982

Qy 1981 ACTGATGCTCAACAAACCTCACAGTCTCCCCCTTCACCTGAACCTTACCTCAGAAGAAAAC 2040
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Db 1983 ACTGATGCTCAACAAACCTCACAGTCTCCCCCTTCACCTGAACCTTACCTCAGAAGAAAAC 2042

Qy 2041 AAAATCCAGATGCTGACAAAGCAAATGAAAAAAAGTTGACCAGCCTCCAGAAGCTAAA 2100
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Qy 2101 AAGCCCAAAATAAAGGTGGTGAATGTTGAGCTGCCTATTGAAGCCAACTTGGTCTGGCAG 2160
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Db 2103 AAGCCCAAAATAAAGGTGGTGAATGTTGAGCTGCCTATTGAAGCCAACTTGGTCTGGCAG 2162

Qy 2161 TTAGGGAAAGACCTTCTTAACATGTATATTGAGACAGAGGGTAAGATGATAATGCAAGAT 2220
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Db 2163 TTAGGGAAAGACCTTCTTAACATGTATATTGAGACAGAGGGTAAGATGATAATGCAAGAT 2222

Qy 2221 AAATTGGAAAAAGAAAGGAATGATGCTAAAAATGCAGTTGAGGAATATGTGTATGAGTTC 2280
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Qy 2281 AGAGACAAGCTGTGTGGACCATATGAAAAATTTATATGTGAGCAGGATCATCAAAATTTT 2340
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Qy 2341 TTGAGACTCCTCACAGAACTGAAGACTGGCTGTATGAAGAAGGAGAGGACCAAGCTAAA 2400
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Db 2343 TTGAGACTCCTCACAGAACTGAAGACTGGCTGTATGAAGAAGGAGAGGACCAAGCTAAA 2402

Qy 2401 CAAGCATATGTTGACAAGTTGGAAGAATTAATGAAAATTGGCACTCCAGTTAAAGTTCGG 2460
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Qy 2461 TTTCAGGAAGCTGAAGAACGGCCAAAAATGTTTGAAGAACTAGGACAGAGGCTGCAGCAT 2520
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Qy 2641 ATGAATGCTCAGGCTAAAAAGAGTCTTGATCAGGATCCAGTTGTACGTGCTCAGGAAATT 2700
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Qy 2761 AAAATTGAATCACCCAAACTGGAAAGAACTCCAAATGGCCCAAATATTGATAAAAAGGAA 2820
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Qy 2821 GAAGATTTAGAAGACAAAAACAATTTTGGTGTGAACCTCCACATCAGAATGGTGAATGT 2880
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Db 2823 GAAGATTTAGAAGACAAAAACAATTTTGGTGTGAACCTCCACATCAGAATGGTGAATGT 2882
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Db 2883 TACCCTAATGAGAAAAATTCTGTTAATATGGACTTGGACTAGATAACCTTAAATTGGCCT 2942
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Qy 2941 ATTCTTCAATTAATAAAATATTTTGGCATAGTATGTGACTCTACATAACATACTGAAA 3000
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Db 2943 ATTCTTCAATTAATAAAATATTTTGGCATAGTATGTGACTCTACATAACATACTGAAA 3002
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Qy 3001 CTATTTATATTTCTTTTAAAGGATATTTAGAAATTTGTGTATTATATGAAAAAGAA 3060
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Db 3003 CTATTTATATTTCTTTTAAAGGATATTTAGAAATTTGTGTATTATATGAAAAAGAA 3062
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Db 3063 AAAAAGCTTAAGTCTGTAGTCTTTATGATCCTAAAAGGGAAAATTGCCTTGGTAACTTTC 3122
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Db 3123 AGATTCTGTGGAATTGTGAATTCATACTAAGCTTTCTGTGCAGTCTCACCATTTCATC 3182
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Db 3183 ACTGAGGATGAAACTGACTTTTGTCTTTTGGAGAAAAAACTGTACTGCTTGTTCAGA 3242
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Qy 3240 GGGCTGTGATTAAAATCTTTAAGCATTGTTCCTGCCAAGGTAGTTTCTTGCAATTTGC 3299
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Qy 3300 TCTCCATTCAAGCATGTGTGTGGGTGTGGATGTTTATAACAAGACTAAGTCTGACTTCAT 3359
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Db 3423 ATTCAATGAGTAAAACAAAAGCTAGTCAAATGTGTTAGCAGCATGCAGAACAAAACTTT 3482
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Qy 3480 AAACCTTCTCTCTCACTATACAGTATATTGTCAATGTGAAAGTGTGGAATGGAAGAAATG 3539
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Qy 3600 TGGTGTCAATTT 3610
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Application/Control Number:
10/525,831
Art Unit: 1643

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Db 3602 TGGTGTCAATTT 3612

RESULT 3

US-09-880-107-1753

; Sequence 1753, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1753
; LENGTH: 3614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 D86956
US-09-880-107-1753

Query Match 99.2%; Score 3583.8; DB 4; Length 3614;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3607; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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Qy     61 GCGGCAGAGTGAGGCAGGCAACCCGAGGTGCGGAGCGACCTGCGGAGGCTGAGCCCCGCT 120
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Db     63 GCGGCAGAGTGAGGCAGGCAACCCGAGGTGCGGAGCGACCTGCGGAGGCTGAGCCCCGCT 122

Qy    121 TTCTCCCAGGGTTTCTTATCAGCCAGCCGCGCTGTCCCCGGGGGAGTAGGAGGCTCCTG 180
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Db    123 TTCTCCCAGGGTTTCTTATCAGCCAGCCGCGCTGTCCCCGGGGGAGTAGGAGGCTCCTG 182

Qy    181 ACAGGCCGCGGCTGTCTGTGTCTTCTGAGTGTCTAGAGGAACGGCCAGACCCGCGGG 240
        |||
Db    183 ACAGGCCGCGGCTGTCTGTGTCTTCTGAGTGTCTAGAGGAACGGCCAGACCCGCGGG 242

Qy    241 CCGGAGCAGAACGCGGCCAGGGCAGAAAGCGGCGGCAGGAGAAGCAGGCAGGGGGCCGGA 300
        |||
Db    243 CCGGAGCAGAACGCGGCCAGGGCAGAAAGCGGCGGCAGGAGAAGCAGGCAGGGGGCCGGA 302

Qy    301 GGACGCAGACCGAGACCCGAGGCGGAGGCGGACCGCGAGCCGGCCATGTCGGTGGTGGGG 360
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Db    303 GGACGCAGACCGAGACCCGAGGCGGAGGCGGACCGCGAGCCGGCCATGTCGGTGGTGGGG 362

Qy    361 TTGGACGTGGGCTCGCAGAGCTGCTACATCGCGGTAGCCCGGGCCGGGGGCATCGAGACC 420
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Db    363 TTGGACGTGGGCTCGCAGAGCTGCTACATCGCGGTAGCCCGGGCCGGGGGCATCGAGACC 422

Qy    421 ATCGCCAATGAGTTTACGCGACCGGTGCACCCCGTCAGTCATATCATTGGATCAAAAAAT 480
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Qy	481	AGAACAATCGGAGTTGTCAGCCAAAAATCAGCAAATCACTCATGCAAACAATACGGTGTCT	540
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Qy	541	AACTTCAAAGATTTTCATGGCCGAGCATTCAACGACCCCTTCATTCAAAGGAGAAGGAA	600
Db	543	AACTTCAAAGATTTTCATGGCCGAGCATTCAATGACCCCTTCATTCAAAGGAGAAGGAA	602
Qy	601	AACTTGAGTTACGATTTGGTTCCATTGAAAAATGGTGGAGTTGGAATAAAGGTAATGTAC	660
Db	603	AACTTGAGTTACGATTTGGTTCCATTGAAAAATGGTGGAGTTGGAATAAAGGTAATGTAC	662
Qy	661	ATGGGTGAAGAACATCTATTTAGTGTGGAGCAGATAACAGCCATGTTGTTGACTAAGCTG	720
Db	663	ATGGGTGAAGAACATCTATTTAGTGTGGAGCAGATAACAGCCATGTTGTTGACTAAGCTG	722
Qy	721	AAGGAAACTGCTGAAAACAGCCTCAAGAAACAGTAACAGATTGTGTTATTTTCAGTCCCC	780
Db	723	AAGGAAACTGCTGAAAACAGCCTCAAGAAACAGTAACAGATTGTGTTATTTTCAGTCCCC	782
Qy	781	TCCTTCTTTACAGATGCTGAGAGGCGATCTGTGTTAGATGCTGCACAGATTGTTGGCCTA	840
Db	783	TCCTTCTTTACAGATGCTGAGAGGCGATCTGTGTTAGATGCTGCACAGATTGTTGGCCTA	842
Qy	841	AACTGTTTAAGACTTATGAATGACATGACAGCTGTTGCTTTGAATTACGGAATTTATAAG	900
Db	843	AACTGTTTAAGACTTATGAATGACATGACAGCTGTTGCTTTGAATTACGGAATTTATAAG	902
Qy	901	CAGGATCTCCCAAGCCTGGATGAGAAACCTCGGATAGTGGTTTTGTGATATGGGACAT	960
Db	903	CAGGATCTCCCAAGCCTGGATGAGAAACCTCGGATAGTGGTTTTGTGATATGGGACAT	962
Qy	961	TCAGCTTTTCAAGTGTCTGCTTGTGCTTTTAAACAAGGAAAAATTGAAGGTACTGGGAACA	1020
Db	963	TCAGCTTTTCAAGTGTCTGCTTGTGCTTTTAAACAAGGAAAAATTGAAGGTACTGGGAACA	1022
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Qy	1081	GCAGAATTTAAAACTAAGTACAAGTTGGATGCAAAATCCAAAATACGAGCACTCCTACGT	1140
Db	1083	GCAGAATTTAAAACTAAGTACAAGTTGGATGCAAAATCCAAAATACGAGCACTCCTACGT	1142
Qy	1141	CTGTATCAGGAATGTGAAAACTGAAAAAGCTAATGAGCTCTAACAGCACAGACCTTCCA	1200
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Qy	1261	TTTGAAGAACTCTGTGCTGAACTTCTGCAAAAGATAGAAGTACCCCTTTATTCACTGTTG	1320
Db	1263	TTTGAAGAACTCTGTGCTGAACTTCTGCAAAAGATAGAAGTACCCCTTTATTCACTGTTG	1322
Qy	1321	GAACAAACTCATCTCAAAGTAGAAGATGTGAGTGCAGTTGAGATTGTTGGAGGCGCTACA	1380
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Qy	1381	CGAATTCAGCTGTGAAGGAAGAATTGCCAAATTCCTTGGAAAAGATATTAGCACAACA	1440
Db	1383	CGAATTCAGCTGTGAAGGAAGAATTGCCAAATTCCTTGGAAAAGATATTAGCACAACA	1442
Qy	1441	CTCAATGCAGATGAAGCAGTAGCCAGAGGATGTGCATTACAGTGTGCAATACTTTCCCG	1500

Db 1443 CTCAATGCAGATGAAGCAGTAGCCAGAGGATGTGCATTACAGTGTGCAATACTTTCCCCG 1502

Qy 1501 GCATTTAAAGTTAGAGAATTTTCCGTACAGATGCAGTTCCTTTTCCAATATCTCTGATC 1560
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Db 1503 GCATTTAAAGTTAGAGAATTTTCCGTACAGATGCAGTTCCTTTTCCAATATCTCTGATC 1562

Qy 1561 TGAACCATGATTTCAGAAGATACTGAAGGTGTTTCATGAAGTCTTTAGTCGAAACCATGCT 1620
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Db 1563 TGAACCATGATTTCAGAAGATACTGAAGGTGTTTCATGAAGTCTTTAGTCGAAACCATGCT 1622

Qy 1621 GCTCCTTTCTCCAAAGTTCTCACCTTTCTGAGAAGGGGGCCTTTTGAGCTAGAAGCTTTC 1680
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Qy 1681 TATTCTGATCCCCAAGGAGTTCCATATCCAGAAGCAAAAATAGGCCGCTTTGTAGTTTCA 1740
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Db 1683 TATTCTGATCCCCAAGGAGTTCCATATCCAGAAGCAAAAATAGGCCGCTTTGTAGTTTCA 1742

Qy 1741 AATGTTTCTGCACAGAAAGATGGAGAAAAATCTAGAGTAAAAGTCAAAGTGCAGTCAAC 1800
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Db 1743 AATGTTTCTGCACAGAAAGATGGAGAAAAATCTAGAGTAAAAGTCAAAGTGCAGTCAAC 1802

Qy 1801 ACCCATGGCATTTTACCCTCTCTACGGCATCTATGGTGGAGAAAGTCCCAACTGAGGAG 1860
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Db 1803 ACCCATGGCATTTTACCCTCTCTACGGCATCTATGGTGGAGAAAGTCCCAACTGAGGAG 1862

Qy 1861 AATGAAATGTCTTCTGAAGCTGACATGGAGTGTCTGAATCAGAGACCACCAGAAAACCA 1920
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Db 1863 AATGAAATGTCTTCTGAAGCTGACATGGAGTGTCTGAATCAGAGACCACCAGAAAACCA 1922

Qy 1921 GACACTGATAAAAAATGTCCAGCAAGACAACAGTGAAGCTGGAACACAGCCCCAGGTACAA 1980
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Db 1923 GACACTGATAAAAAATGTCCAGCAAGACAACAGTGAAGCTGGAACACAGCCCCAGGTACAA 1982

Qy 1981 ACTGATGCTCAACAAACCTCACAGTCTCCCCCTTACCTGAACCTTACCTCAGAAGAAAAC 2040
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Db 1983 ACTGATGCTCAACAAACCTCACAGTCTCCCCCTTACCTGAACCTTACCTCAGAAGAAAAC 2042

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Db 2043 AAAATCCAGATGCTGACAAAGCAAATGAAAAAAAGTTGACCAGCCTCCAGAAGCTAAA 2102

Qy 2101 AAGCCCAAAATAAAGGTGGTGAATGTTGAGCTGCCTATTGAAGCCAACTTGGTCTGGCAG 2160
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Db 2103 AAGCCCAAAATAAAGGTGGTGAATGTTGAGCTGCCTATTGAAGCCAACTTGGTCTGGCAG 2162

Qy 2161 TTAGGGAAAGACCTTCTTAACATGTATATTGAGACAGAGGGTAAGATGATAATGCAAGAT 2220
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Db 2163 TTAGGGAAAGACCTTCTTAACATGTATATTGAGACAGAGGGTAAGATGATAATGCAAGAT 2222

Qy 2221 AAATTGGAAAAAGAAAGGAATGATGCTAAAAATGCAGTTGAGGAATATGTGTATGAGTTC 2280
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Db 2223 AAATTGGAAAAAGAAAGGAATGATGCTAAAAATGCAGTTGAGGAATATGTGTATGAGTTC 2282

Qy 2281 AGAGACAAGCTGTGTGGACCATATGAAAAATTTATATGTGAGCAGGATCATCAAAATTTT 2340
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Db 2283 AGAGACAAGCTGTGTGGACCATATGAAAAATTTATATGTGAGCAGGATCATCAAAATTTT 2342

Qy 2341 TTGAGACTCCTCACAGAACTGAAGACTGGCTGTATGAAGAAGGAGAGGACCAAGCTAAA 2400
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Db 2343 TTGAGACTCCTCACAGAACTGAAGACTGGCTGTATGAAGAAGGAGAGGACCAAGCTAAA 2402

Qy 2401 CAAGCATATGTTGACAAGTTGGAAGAATTAATGAAAATTTGGCACTCCAGTTAAAGTTCGG 2460
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Db 2403 CAAGCATATGTTGACAAGTTGGAAGAATTAATGAAAATTTGGCACTCCAGTTAAAGTTCGG 2462

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Db	2463	TTTCAGGAAGCTGAAGAACGGCCAAAAATGTTTGAAGAACTAGGACAGAGGCTGCAGCAT	2522
Qy	2521	TATGCCAAGATAGCAGCTGACTTCAGAAATAAGGATGAGAAATACAACCATATTGATGAG	2580
Db	2523	TATGCCAAGATAGCAGCTGACTTCAGAAATAAGGATGAGAAATACAACCATATTGATGAG	2582
Qy	2581	TCTGAAATGAAAAAGTGGAGAAGTCTGTTAATGAAGTGATGGAATGGATGAATAATGTC	2640
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Db	2763	AAAATTGAATCACCCAACTGGAAAGAAGTCCAAATGGCCCAAATATTGATAAAAAAGGAA	2822
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Qy	3061	AAAAAGCTTAAGTCTGTAGTCTTTATGATCCTAAAAGGAAAAATTGCCTTGTTAACTTTC	3120
Db	3063	AAAAAGCTTAAGTCTGTAGTCTTTATGATCCTAAAAGGAAAAATTGCCTTGTTAACTTTC	3122
Qy	3121	AGATTCTGTGGAATTGTGAATTCATACTAAGCTTTCTGTGCAGTCTCACCATTTCATC	3180
Db	3123	AGATTCTGTGGAATTGTGAATTCATACTAAGCTTTCTGTGCAGTCTCACCATTTCATC	3182
Qy	3181	ACTGAGGATGAAACTGACTTTTGTCTTTTGGAGAAAAAACTGTACTG-TGTTCAAGA	3239
Db	3183	ACTGAGGATGAAACTGACTTTTGTCTTTTGGAGAAAAAACTGTACTGCTTGTTCAGA	3242
Qy	3240	GGGCTGTGATTAAATCTTTAAGCATTTGTTCTGCGCAAGGTAGTTTTCTTGCATTTTGC	3299
Db	3243	GGGCTGTGATTAAATCTTTAAGCATTTGTTCTGCGCAAGGTAGTTTTCTTGCATTTTGC	3302
Qy	3300	TCTCCATTCAGCATGTGTGTGGGTGTGGATGTTTATAAACAAGACTAAGTCTGACTTCAT	3359
Db	3303	TCTCCATTCAGCATGTGTGTGGGTGTGGATGTTTATAAACAAGACTAAGTCTGACTTCAT	3362
Qy	3360	AAGGGCTTTCTAAAACCATTTCTGTCCAAGAGAAAAATGACTTTTTGCTTTGATATTAAAA	3419
Db	3363	AAGGGCTTTCTAAAACCATTTCTGTCCAAGAGAAAAATGACTTTTTGCTTTGATATTAAAA	3422
Qy	3420	ATTCAATGAGTAAACAAAAGCTAGTCAAATGTGTTAGCAGCATGCAGAACAAAACTTT	3479

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Db      3423 ATTCAATGAGTAAAACAAAAGCTAGTCAAATGTGTTAGCAGCATGCAGAACAAAACTTT 3482
Qy      3480 AAACTTTCTCTCTCACTATACAGTATATTGTCAATGTGAAAGTGTGGAATGGAAGAAATG 3539
        |||
Db      3483 AAACTTTCTCTCTCACTATACAGTATATTGTC-ATGTGAAAGTGTGGAATGGAAGAAATG 3541
Qy      3540 TCGATCCTGTTGTAAGTGAACACTTTTATGAGCTTTAAAAATAAAGTTCATCTTA 3599
        |||
Db      3542 TCGATCCTGTTGTAAGTGAACACTTTTATGAGCTTTAAAAATAAAGTTCATCTTA 3601
Qy      3600 TGGTGTCAATTT 3610
        |||
Db      3602 TGGTGTCAATTT 3612
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Conclusion

No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Anne Holleran, whose telephone number is (571) 272-0833. The examiner can normally be reached on Monday through Friday from 9:30 am to 5:00 pm. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Larry Helms, can be reached on (571) 272-0832. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (571) 272-1600.

Papers related to this application may be submitted to Group 1600 by facsimile transmission. The faxing of such papers must conform to the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989). The Official Fax number for Group 1600 is (571) 273-8300.

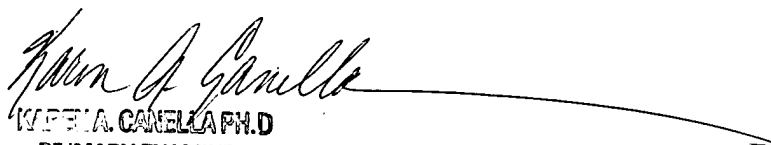
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Anne L. Holleran
Patent Examiner
December 26, 2007


W. P. M. CANELLA PH.D
PRIMARY EXAMINER